

PCT
KW

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,994

DATE: 06/07/2001
TIME: 09:22:21

Input Set : A:\DES.txt
Output Set: C:\CRF3\06072001\I830994.raw

3 <110> APPLICANT: YLIHONKO, Kristiina
4 RAETY, Kaj
5 HAKALA, Juha
7 <120> TITLE OF INVENTION: THE GENE CLUSTER INVOLVED IN ACLACINOMYCIN BIOSYNTHESIS, AND
ITS USE FOR
8 GENETIC ENGINEERING
10 <130> FILE REFERENCE: 1574/49884
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/830,994
C--> 12 <141> CURRENT FILING DATE: 2000-09-25
12 <150> PRIOR APPLICATION NUMBER: PCT/FI00/00819
13 <151> PRIOR FILING DATE: 2000-09-25
15 <160> NUMBER OF SEQ ID NOS: 16
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 662
21 <212> TYPE: PRT
22 <213> ORGANISM: Streptomyces galilaeus
24 <400> SEQUENCE: 1
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27 1 5 10 15
29 Leu Ala Pro Leu Leu Asp Gly Ser Arg Asp Leu Pro Gly Ile Val Ala
30 20 25 30
32 Asp Ala Ala Pro Arg Leu Pro Ala Gly Leu Ala Glu Arg Leu Val Thr
33 35 40 45
35 Arg Leu Leu Asp Ala Gly Leu Leu Cys Ala Tyr Pro Gln Asp Gly Ala
36 50 55 60
38 Asp Arg Pro Glu Arg Ala Tyr Arg Ser Leu Thr Gly Leu Gln Ala Arg
39 65 70 75 80
41 Ser Ala Asp Ala Arg Asp Ala Val Leu Ala Ala Val Asp Leu Thr Gly
42 85 90 95
44 Asp Ala Glu Ser Pro Leu Pro Glu Ala Val Ser Ala Ala Gly Leu Arg
45 100 105 110
47 Ala Ala Ala Pro Gly Glu His Ala Ala Leu Thr Leu Val Leu Cys His
48 115 120 125
50 Asp Tyr Leu Asp Pro Arg Leu Ser Ala Leu Asp Ala Glu His Arg Ala
51 130 135 140
53 Thr Gly Arg Gly Trp Leu Pro Val Arg Ala Asn Gly Thr His Leu Trp
54 145 150 155 160
56 Ile Gly Pro Phe Phe Ser Ala Gly Asp Gly Pro Cys Trp Ser Cys Leu
57 165 170 175
59 Ala Asp Arg Leu Arg Leu Arg Arg Gly Glu Ala Tyr Val Gln His
60 180 185 190
62 Arg Leu Gly His Ser Gly Pro Ala Val His Arg Arg Ala Tyr Leu Pro
63 195 200 205
65 Ala Gly Arg Ala Ala Ala Leu Gln Leu Ala Leu Leu Glu Ala Gly Lys
66 210 215 220
68 Trp Leu Ser Gly His Arg Asp Thr Val Gln Asp Ser Leu Trp Arg Leu
69 225 230 235 240

ENTERED

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71 Asp Thr Arg Thr Leu Glu Ser Ser Arg His Pro Val Arg Arg Arg Pro
 72 245 250 255
 74 Gln Cys Ser Arg Cys Gly Asp Pro Leu Leu Val Arg Asp Arg Val Ser
 75 260 265 270
 77 Ala Pro Val Val Leu Ser Ser Arg Pro Val Arg Asp Glu Ser Gly Gly
 78 275 280 285
 80 Gly His Arg Thr Phe Gly Pro Gln Glu Met Leu Asp Arg Tyr Gly His
 81 290 295 300
 83 Leu Val Asp Pro Val Thr Gly Val Val Gly Glu Ile Arg Arg Asp Pro
 84 305 310 315 320
 86 Arg Gly Pro Glu Phe Leu Asn Cys Phe Thr Arg Ser Arg Cys Arg Leu
 87 325 330 335
 89 Gly Pro Arg Ala Ala Pro Pro Ala Leu His Ser Pro Leu Arg Ser Pro
 90 340 345 350
 92 Gly Ser Gly Lys Gly Val Thr Glu Leu His Ala Arg Val Ser Ala Leu
 93 355 360 365
 95 Ala Glu Ala Leu Glu Arg Cys Ser Gly Tyr Phe Gln Gly Asp Glu Pro
 96 370 375 380
 98 Arg Arg Arg Gly Ser Tyr Arg Glu Leu Ala Gly Leu Ala Val His Pro
 99 385 390 395 400
 101 Asp Ser Val Gln Leu Phe Asp Arg Arg Gln Phe Glu Asp Arg Arg Ala
 102 405 410 415
 104 Trp Asn Arg Ala His Gly Pro Phe His Gln Val Thr Glu Pro Phe Asp
 105 420 425 430
 107 Glu Asp Ala Pro Ile Asp Trp Thr Pro Val Trp Ser Leu Thr Glu Arg
 108 435 440 445
 110 Arg Gln Arg Leu Ala Pro Thr Ser Leu Leu Tyr Tyr Asn Ala Pro Asp
 111 450 455 460
 113 Ala Asp Thr Gly Phe Cys Arg Ala Thr Ser Asn Gly Ala Ala Ala Gly
 114 465 470 475 480
 116 Thr Ser Leu Glu Asp Ala Val Val His Gly Cys Leu Glu Leu Val Glu
 117 485 490 495
 119 Arg Asp Ala Ile Ala Leu Trp Trp Tyr Asn Arg Thr Arg Gln Pro Gly
 120 500 505 510
 122 Val Thr Leu Asp Ala Arg Asp Pro Trp Ile Thr Arg Leu Arg Ala Val
 123 515 520 525
 125 Leu Arg Asp Leu Gly Arg Thr Val Trp Ala Leu Asp Leu Thr Ser Asp
 126 530 535 540
 128 Leu Gly Ile Pro Val Val Ala Ala Val Ser Val Arg Thr Gly Gly Thr
 129 545 550 555 560
 131 Ala Glu Asp Ile Val Leu Gly Phe Gly Ala His Phe Asp Pro Arg Ile
 132 565 570 575
 134 Ala Leu Arg Arg Ala Leu Thr Glu Leu Ser Gln Met Leu Pro Pro Leu
 135 580 585 590
 137 Ala Gln Glu Thr Ala Gly Asp Ala Ser Ala Tyr Thr Gly Thr Asp Pro
 138 595 600 605
 140 Glu Ala Met Arg Trp Phe Arg His Ala Thr Thr Ala Asn Gln Pro Tyr
 141 610 615 620
 143 Leu Leu Pro Ala Ala Arg Arg Ser Ala Arg Pro Pro Ala Ser Leu Arg

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144 625 630 635 640
146 Pro Pro Arg Asp Ala Ala Ala Gln Ala Gly Ala Leu Val Ala Leu Leu
147 645 650 655
149 Arg Arg His Gly Leu Glu
150 660
152 <210> SEQ ID NO: 2
153 <211> LENGTH: 272
154 <212> TYPE: PRT
155 <213> ORGANISM: Streptomyces galilaeus
157 <400> SEQUENCE: 2
159 Val Asp Ile Trp Leu Leu Gly Pro Leu Thr Ala Glu Val Arg Gly Arg
160 1 5 10 15
162 Ser Ile Val Pro Thr Ala Ala Lys Pro Arg Gln Ile Leu Ala Leu Leu
163 20 25 30
165 Ala Ile His Ala Asn Arg Val Leu Pro Val Gly Thr Leu Met Glu Glu
166 35 40 45
168 Ile Trp Gly Thr Glu Pro Pro Gln Ser Ala Leu Ala Thr Leu His Thr
169 50 55 60
171 Tyr Ile Leu Gln Leu Arg Arg Arg Leu Thr Ala Ala Tyr Gly Asp Glu
172 65 70 75 80
174 Gly Gly Val Ser Ala Lys Asp Val Leu Val Thr Gln Tyr Gly Gly Tyr
175 85 90 95
177 Cys Trp Gln Ala Pro Thr Asp Ser Val Asp Val Pro Arg Tyr Glu Arg
178 100 105 110
180 Leu Val Thr Ala Gly Arg Ile Ala Thr Ala Glu Asp Arg Gln Glu Glu
181 115 120 125
183 Ala Ser Ala His Phe Arg Glu Ala Leu Ala Leu Trp Arg Gly Ser Ala
184 130 135 140
186 Leu Val Asp Val Arg Ile Gly Pro Val Leu Ser Ile Glu Val Ala Arg
187 145 150 155 160
189 Leu Glu Glu Ser Arg Leu Gly Val Leu Glu Arg Cys Leu Glu Ala Asp
190 165 170 175
192 Leu Arg Leu Gly Arg His Ala Glu Leu Leu Ala Glu Leu Thr Glu Leu
193 180 185 190
195 Thr Gly Arg His Pro Leu His Glu Gly Leu His Ala Gln Cys Met Thr
196 195 200 205
198 Ala Leu Tyr Arg Ala Gly Arg Ser Trp Gln Ala Leu Asp Val Tyr Gln
199 210 215 220
201 Arg Leu Arg Arg Arg Leu Ala Glu Glu Leu Gly Leu Ser Pro Ser Pro
202 225 230 235 240
204 Arg Leu Gln Arg Leu Gln Gln Ala Val Leu Ser Ala Glu Pro Trp Leu
205 245 250 255
207 Asp Ala Pro Arg Tyr Gly Gly Asp Pro Val Phe Asp Arg Met Ile Ser
208 260 265 270
210 <210> SEQ ID NO: 3
211 <211> LENGTH: 434
212 <212> TYPE: PRT
213 <213> ORGANISM: Streptomyces galilaeus
215 <400> SEQUENCE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,994

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217 Met Thr Ser Asp Thr Lys Ala Leu Val Leu Glu Gln Val Arg Glu Tyr
 218 1 5 10 15
 220 His Arg Gln Gln Gln Pro Gly Asn Phe Gln Pro Gly Val Thr Pro Ile
 221 20 25 30
 223 Leu Ser Ser Gly Ala Val Leu Asp Glu Glu Asp Arg Val Ala Leu Val
 224 35 40 45
 226 Glu Ala Ala Leu Asp Leu Arg Ile Ala Ala Gly Ala His Ser Arg Arg
 227 50 55 60
 229 Phe Glu Ser Lys Phe Ala Arg His Ile Gly Val Arg Lys Ala His Leu
 230 65 70 75 80
 232 Val Asn Ser Gly Ser Ser Ala Asn Leu Leu Ala Leu Ser Ala Leu Thr
 233 85 90 95
 235 Ser Pro Arg Leu Gly Glu Gln Arg Leu Arg Pro Gly Asp Glu Val Ile
 236 100 105 110
 238 Thr Val Ala Gly Gly Phe Pro Thr Thr Val Asn Pro Ile Leu Gln Asn
 239 115 120 125
 241 Gly Leu Thr Pro Val Phe Val Asp Leu Glu Leu Gly Thr Tyr Asn Thr
 242 130 135 140
 244 Thr Val Glu His Val Arg Ala Ala Ile Ser Asp Arg Thr Arg Ala Ile
 245 145 150 155 160
 247 Met Ile Ala His Thr Leu Gly Asn Pro Tyr Gln Val Ala Glu Ile Gln
 248 165 170 175
 250 Gln Leu Ala Thr Glu His Glu Leu Phe Leu Ile Glu Asp Asn Cys Asp
 251 180 185 190
 253 Ala Val Gly Ser Thr Tyr Gln Gly Arg Met Thr Gly Thr Phe Gly Asp
 254 195 200 205
 256 Leu Ala Thr Val Ser Phe Tyr Pro Ala His His Ile Thr Thr Gly Glu
 257 210 215 220
 259 Gly Gly Cys Val Leu Thr Arg Asn Leu Glu Leu Ala Arg Ile Val Glu
 260 225 230 235 240
 262 Ser Phe Arg Asp Trp Gly Arg Asp Cys Trp Cys Glu Pro Gly Glu Asp
 263 245 250 255
 265 Asn Thr Cys Leu Lys Arg Phe Asp Tyr Gln Leu Gly Asn Leu Pro Lys
 266 260 265 270
 268 Gly Tyr Asp His Lys Tyr Ile Phe Ser His Ile Gly Tyr Asn Leu Lys
 269 275 280 285
 271 Ala Thr Asp Leu Gln Gly Ala Leu Ala Leu Ser Gln Leu Asn Lys Leu
 272 290 295 300
 274 Pro Glu Phe Gly Ala Ala Arg Arg Asn Trp Gln Arg Leu Arg Asp
 275 305 310 315 320
 277 Gly Leu Ala Asp Val Pro Gly Leu Leu Leu Pro Val Ala Thr Pro Gly
 278 325 330 335
 280 Ser Asp Pro Ser Trp Phe Gly Phe Val Ile Thr Val Leu Pro Asp Ala
 281 340 345 350
 283 Thr Tyr Thr Arg Arg Asp Leu Val Ala Phe Leu Glu Glu Arg Arg Ile
 284 355 360 365
 286 Gly Thr Arg Arg Leu Phe Gly Gly Asn Leu Thr Arg His Pro Ala Tyr
 287 370 375 380
 289 Leu Gly Thr Pro His Arg Val Ala Gly Asp Leu Arg Asn Ser Asp Ile

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290	385	390	395	400												
292	Ile	Thr	Glu	Gln	Ser	Phe	Trp	Ile	Gly	Val	Tyr	Pro	Gly	Ile	Thr	Glu
293																415
																410
295	Glu	Met	Thr	Asp	Tyr	Met	Arg	Glu	Ser	Ile	Val	Glu	Phe	Val	Thr	Lys
296																425
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298	Asn	Gly														
301	<210>	SEQ	ID	NO:	4											
302	<211>	LENGTH:	329													
303	<212>	TYPE:	PRT													
304	<213>	ORGANISM:	Streptomyces galilaeus													
306	<400>	SEQUENCE:	4													
308	Met	Pro	Lys	Asp	Thr	Pro	Arg	Pro	Val	Leu	Arg	Ile	Gly	Val	Leu	Gly
309	1															15
																10
311	Cys	Ala	Asp	Ile	Ala	Val	Arg	Arg	Ile	Leu	Pro	Ala	Ile	Val	Glu	His
312																30
																25
314	Pro	Ser	Val	Arg	Leu	Val	Ala	Leu	Ala	Ser	Arg	Asp	Gly	Ala	Arg	Ala
315																45
																35
317	Glu	Arg	Leu	Ala	Ala	Arg	Phe	Gly	Cys	Ala	Ala	Val	Thr	Gly	Tyr	Lys
318																60
																50
320	Ala	Leu	Leu	Asp	Arg	Glu	Asp	Ile	Asn	Ala	Val	Tyr	Val	Pro	Leu	Pro
321																80
																70
323	Pro	Gly	Met	His	His	Glu	Trp	Val	Thr	Glu	Ala	Leu	Thr	Ala	Gly	Lys
324																95
																85
326	His	Val	Leu	Val	Glu	Lys	Pro	Leu	Ser	Thr	Thr	Tyr	Ala	Gln	Ser	Val
327																110
																100
329	Asp	Leu	Val	Ala	Met	Ala	Gly	Arg	Leu	Gly	Leu	Ala	Leu	Thr	Glu	Asn
330																125
																115
332	Phe	Met	Phe	Leu	His	His	Ser	Gln	His	Glu	Ala	Val	Arg	Ala	Met	Thr
333																140
																130
335	Gly	Glu	Ile	Gly	Glu	Leu	Arg	Val	Phe	Thr	Ser	Ser	Phe	Gly	Val	Pro
336	145															160
																150
338	Pro	Pro	His	Pro	Ser	Ser	Phe	Arg	His	Asp	Ala	Arg	Leu	Gly	Gly	Gly
339																175
																165
341	Ala	Leu	Leu	Asp	Val	Gly	Val	Tyr	Pro	Leu	Arg	Ala	Ala	Gln	Leu	His
342																190
																180
344	Leu	Ala	Gly	Glu	Leu	Asp	Val	Leu	Gly	Ala	Cys	Leu	Arg	Val	Asp	Glu
345																205
																195
347	Ala	Thr	Gly	Val	Asp	Val	Ala	Gly	Ser	Ala	Leu	Leu	Ser	Thr	Ala	Thr
348																220
																210
350	Gly	Val	Thr	Ala	Gln	Leu	Asp	Phe	Gly	Phe	Gln	His	Ala	Tyr	Arg	Ser
351	225															240
																230
353	Val	Tyr	Ala	Leu	Trp	Gly	Ser	Arg	Gly	Arg	Leu	Ser	Val	Pro	Arg	Ala
354																255
																245
356	Phe	Thr	Pro	Pro	Arg	Glu	His	Arg	Pro	Val	Val	Arg	Ile	Glu	Gln	Gln
357																270
																260
359	Asp	Arg	Leu	Thr	Glu	Val	Thr	Leu	Pro	Ala	Asp	His	Gln	Val	Gly	Asn
360																285
																275
362	Ala	Leu	Asp	Ala	Phe	Ala	Ser	Ala	Val	His	Ser	Glu	Thr	Val	Arg	Ala
363																300
																295

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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TIME: 09:22:22

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

L:1472 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15

L:1485 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16